

SEQUENCE LISTING

10/516662
#9
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<110> University of Utah Research Foundation
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Hobden, Adrian N.

<120> VARIANTS OF ANTITHROMBIN III

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<150> 60/384,599

<151> 2002-05-31

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20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100 105 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115 120 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr

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Thr	Val	Leu	195	Val	Leu	Val	Asn	200	Thr	Ile	Tyr	Phe	Lys	205	Gly	Leu	Trp	Lys
Ser	Lys	Phe	Ser	Pro	Glu	Asn	215	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala	240	Phe
Asp	Gly	Glu	Ser	Cys	230	Ser	Ala	Ser	Met	250	Tyr	Gln	Glu	Gly	Lys	255	Phe	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	265	Gln	Val	Leu	Glu	Leu	Pro	Phe		
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Ser	Leu	Ala	Lys	Val	Glu	Lys	295	Glu	Leu	Thr	Pro	Glu	300	Val	Leu	Gln	Glu	
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	315	Val	His	Met	Pro	Arg	320	
Phe	Arg	Ile	Glu	Asp	325	Gly	Phe	Ser	Leu	Lys	330	Glu	Gln	Leu	Gln	Asp	335	Met
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Ala	Leu	Glu	Ala	Asn	Gly	390	Arg	Ser	Leu	Asn	Pro	395	Asn	Arg	Val	Thr	Phe	400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	410	Arg	Glu	Val	Pro	Leu	Asn	415	
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20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
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Leu	Gln	Gln	Leu	85	Met	Glu	Val	Phe	Lys	90	Phe	Asp	Thr	Ile	Ser	95	Glu	Lys
Thr	Ser	Asp	100	Gln	Ile	His	Phe	Phe	105	Phe	Ala	Lys	Leu	Asn	110	Cys	Arg	Leu
Tyr	Arg	115	Lys	Ala	Asn	Lys	Ala	120	Ser	Lys	Leu	Val	Ser	125	Ala	Asn	Arg	Leu
Phe	Gly	130	Asp	Lys	Ser	Leu	Thr	135	Phe	Asn	Glu	Thr	Tyr	140	Gln	Asp	Ile	Ser
145	Glu	Leu	Val	Tyr	Gly	150	Ala	Lys	Leu	Gln	Pro	Leu	Asp	155	Phe	Lys	Glu	Asn
Ala	Glu	Gln	Ser	160	Arg	Ala	Ala	Ile	Asn	165	Lys	Trp	Val	Ser	170	Asn	Lys	Thr
Glu	Gly	Arg	180	Ile	Thr	Asp	Val	Ile	Pro	185	Ser	Glu	Ala	Ile	200	Asn	Glu	Leu
Thr	Val	195	Leu	Val	Leu	Val	Asn	200	Thr	Ile	Tyr	Phe	Lys	Gly	205	Leu	Trp	Lys
Ser	Lys	Phe	Ser	Pro	Glu	Asn	210	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	215	Lys	Ala	240
Asp	Gly	Glu	Ser	Cys	225	Ser	Ala	Ser	Met	230	Met	Tyr	Gln	Glu	Gly	Lys	Phe	255
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	245	Val	Leu	Glu	Leu	Pro	Phe	270	285
Lys	Gly	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	250	Pro	Lys	Pro	Glu	Lys	280	295	300
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	265	Pro	Glu	Val	Leu	Gln	Glu	305	315
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	275	Val	Val	His	Met	Pro	Arg	320	325
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	285	Glu	Gln	Leu	Gln	Asp	Met	330	335
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	295	Ser	Lys	Leu	Pro	Gly	Ile	340	345
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	300	Ser	Asp	Ala	Phe	His	Lys	350	355
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	310	Glu	Ala	Ala	Ala	Ser	Thr	360	365
Ala	Leu	Glu	Ala	Gln	Gly	Arg	Ser	Leu	Asn	325	Pro	Asn	Arg	Val	Thr	Phe	370	375
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	330	Arg	Glu	Val	Pro	Leu	Asn	380	385
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	340	Pro	Cys	Val	Lys	400	415	420	425

<210> 78

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 78

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1				5					10				15		
Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
			35				40					45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
			50			55					60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser

246416_1.txt

```

65      70      75      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
      85      90      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
      100      105      110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
      115      120      125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
      130      135      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
      145      150      155
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
      160      165      170
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
      175      180      185
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
      190      195      200
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
      205      210      215
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
      220      225      230
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
      235      240      245
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
      250      255      260
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
      265      270      275
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
      280      285      290
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
      295      300      305
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
      310      315      320
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
      325      330      335
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
      340      345      350
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
      355      360      365
Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
      370      375      380
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
      385      390      395
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
      400      405      410
      415      420      425      430

```

<210> 79

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 79

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agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccgag      120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc      180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt      240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg      300
atggaggtat ttaagtattga caccatatct gagaaaaacat ctgatcagat ccacttcttc      360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca      420

```

246416_1.txt

```

gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
gagttgggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540
agagcgcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacacccat ttacttcaag 660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatgggtc 840
ctcatcttgc ccaagcctga gaagagcctg gccaaaggtgg agaaggaact caccacagag 900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tgggtgtcca catgccccgc 960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat 1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc 1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260
atgggcagag tagccaaccc ttgtgttaag taa 1293

```

<210> 80

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 80

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agtccccgtag atatatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatccccggag 120
gccaccaaac ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc 360
tttgccaaac tgaactgccc actctatcga aaagccaaca aagcctccaa gttagtatca 420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
gatgtggagt atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540
agagcgcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacacccat ttacttcaag 660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatgggtc 840
ctcatcttgc ccaagcctga gaagagcctg gccaaaggtgg agaaggaact caccacagag 900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tgggtgtcca catgccccgc 960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat 1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc 1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260
atgggcagag tagccaaccc ttgtgttaag taa 1293

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<210> 81

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 81

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Ser Pro Val Asp Val Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1      5      10      15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20      25      30

```

246416_1.txt

Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Val	Trp	Glu
		35					40				45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His
	50					55					60			
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu
	65				70					75				80
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp
				85					90				95	
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu
			100					105					110	
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu
		115				120					125			
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg
	130					135					140			
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile
	145				150					155				160
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu
				165					170				175	
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys
			180					185					190	
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu
		195					200					205		
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp
	210					215					220			
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys
	225				230					235				240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys
				245					250				255	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro
			260					265					270	
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu
		275				280						285		
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln
	290					295					300			
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro
	305				310					315				320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp
				325					330				335	
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly
			340					345					350	
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His
		355					360					365		
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser
	370					375					380			
Ala	Leu	Glu	Ala	Gln	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr
	385				390					395				400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu
				405					410				415	
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys	
			420					425					430	

<210> 82

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 82

agccctgtgg acgtatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt

60

246416_1.txt

taccgctccc	cggagaagaa	ggcaactgag	gatgagggct	cagaacagaa	gatccccggag	120
gccaccaacc	ggcgtgtctg	ggaactgtcc	aaggccaatt	cccgccttgc	taccactttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acccttgagt	240
atctccacgg	cttttgctat	gaccaagctg	ggtgcctgta	atgacaccct	ccagcaactg	300
atggaggtat	ttaagtttga	caccatatct	gagaaaacat	ctgatcagat	ccacttcttc	360
tttgccaaac	tgaactgccg	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttgagga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcggcc	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gctcactggt	ctggtgctgg	ttaacaccat	ttacttcaag	660
ggcctgtgga	agtcaaagtt	cagccctgag	aacacaagga	aggaactggt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatgggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaaggtgg	agaaggaact	cacccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtgggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgctgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggtattgttg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgttcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

<210> 83

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 83

agtcccgtag	atgtgtgcac	agccaagccg	cgggacattc	ccatgaatcc	catgtgcatt	60
taccgctccc	cggagaagaa	ggcaactgag	gatgagggct	cagaacagaa	gatccccggag	120
gccaccaacc	ggcgtgtctg	ggaactgtcc	aaggccaatt	cccgccttgc	taccactttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acccttgagt	240
atctccacgg	cttttgctat	gaccaagctg	ggtgcctgta	atgacaccct	ccagcaactg	300
atggaggtat	ttaagtttga	caccatatct	gagaaaacat	ctgatcagat	ccacttcttc	360
tttgccaaac	tgaactgccg	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttgagga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcggcc	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gctcactggt	ctggtgctgg	ttaacaccat	ttacttcaag	660
ggcctgtgga	agtcaaagtt	cagccctgag	aacacaagga	aggaactggt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatgggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaaggtgg	agaaggaact	cacccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtgggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgctgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggtattgttg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgttcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

<210> 84

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

246416_1.txt

<400> 84

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Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1      5      10      15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20      25      30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35      40      45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50      55      60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65      70      75      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85      90      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100      105      110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115      120      125

Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130      135      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145      150      155      160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165      170      175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180      185      190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195      200      205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210      215      220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225      230      235      240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245      250      255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260      265      270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275      280      285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290      295      300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305      310      315      320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
325      330      335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
340      345      350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
355      360      365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
370      375      380
Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385      390      395      400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
405      410      415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420      425      430

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<210> 85

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 85

His 1	Gly	Ser	Pro	Val 5	Asp	Ile	Cys	Thr	Ala 10	Lys	Pro	Arg	Asp	Ile 15	Pro
Met	Asn	Pro	Met 20	Cys	Ile	Tyr	Arg	Ser 25	Pro	Glu	Lys	Lys	Ala 30	Thr	Glu
Asp	Glu	Gly 35	Ser	Glu	Gln	Lys	Ile 40	Pro	Glu	Ala	Thr	Asn 45	Arg	Arg	Val
Trp 50	Glu	Leu	Ser	Lys	Ala	Asn 55	Ser	Arg	Phe	Ala	Thr 60	Thr	Phe	Tyr	Gln
His 65	Leu	Ala	Asp	Ser	Lys 70	Asn	Asp	Asn	Asp 75	Ile	Phe	Leu	Ser	Pro 80	
Leu	Ser	Ile	Ser	Thr 85	Ala	Phe	Ala	Met	Thr 90	Lys	Leu	Gly	Ala	Cys 95	Asn
Asp	Thr	Leu	Gln 100	Gln	Leu	Met	Glu	Val 105	Phe	Lys	Phe	Asp	Thr 110	Ile	Ser
Glu	Lys	Thr 115	Ser	Asp	Gln	Ile	His 120	Phe	Phe	Ala	Lys 125	Leu	Asn	Cys	
Arg 130	Leu	Tyr	Arg	Lys	Ala	Asn 135	Lys	Ser	Ser	Lys	Leu 140	Val	Ser	Ala	Asn
Arg 145	Leu	Phe	Gly	Asp	Lys 150	Ser	Leu	Thr	Phe	Asn 155	Glu	Thr	Tyr	Gln	Asp 160
Ile	Ser	Glu	Leu	Val 165	Tyr	Gly	Ala	Lys	Leu 170	Gln	Pro	Leu	Asp	Phe 175	Lys
Glu	Asn	Ala	Glu 180	Gln	Ser	Arg	Ala	Ala 185	Ile	Asn	Lys	Trp	Val 190	Ser	Asn
Lys	Thr	Glu 195	Gly	Arg	Ile	Thr	Asp 200	Val	Ile	Pro	Ser	Glu 205	Ala	Ile	Asn
Glu 210	Leu	Thr	Val	Leu	Val	Leu 215	Val	Asn	Thr	Ile	Tyr 220	Phe	Lys	Gly	Leu
Trp 225	Lys	Ser	Lys	Phe	Ser 230	Pro	Glu	Asn	Thr	Arg 235	Lys	Glu	Leu	Phe	Tyr 240
Lys	Ala	Asp	Gly	Glu 245	Ser	Cys	Ser	Ala	Ser 250	Met	Met	Tyr	Gln	Glu 255	Gly
Lys	Phe	Arg	Tyr 260	Arg	Arg	Val	Ala	Glu 265	Gly	Thr	Gln	Val	Leu 270	Glu	Leu
Pro	Phe	Lys 275	Gly	Asp	Asp	Ile	Thr 280	Met	Val	Leu	Ile	Leu 285	Pro	Lys	Pro
Glu	Lys	Ser	Leu	Ala	Lys	Val 295	Glu	Lys	Glu	Leu	Thr 300	Pro	Glu	Val	Leu
Gln 305	Glu	Trp	Leu	Asp	Glu 310	Leu	Glu	Glu	Met	Met 315	Leu	Val	Val	His	Met 320
Pro	Arg	Phe	Arg	Ile 325	Glu	Asp	Gly	Phe	Ser 330	Leu	Lys	Glu	Gln	Leu 335	Gln
Asp	Met	Gly	Leu 340	Val	Asp	Leu	Phe	Ser 345	Pro	Glu	Lys	Ser	Lys 350	Leu	Pro
Gly	Ile	Val 355	Ala	Glu	Gly	Arg	Asp 360	Asp	Leu	Tyr	Val	Ser 365	Asp	Ala	Phe
His 370	Lys	Ala	Phe	Leu	Glu	Val 375	Asn	Glu	Glu	Gly	Ser 380	Glu	Ala	Ala	Ala
Ser 385	Thr	Ala	Leu	Glu	Ala 390	Gln	Gly	Arg	Ser	Leu 395	Asn	Pro	Asn	Arg	Val 400
Thr	Phe	Lys	Ala	Asn 405	Arg	Pro	Phe	Leu	Val 410	Phe	Ile	Arg	Glu	Val 415	Pro
Leu	Asn	Thr	Ile 420	Ile	Phe	Met	Gly	Arg 425	Val	Ala	Asn	Pro	Cys 430	Val	Lys

<210> 86

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 86

His 1	Gly	Ser	Pro	Val 5	Asp	Ile	Cys	Thr	Ala 10	Lys	Pro	Arg	Asp	Ile 15	Pro
Met	Asn	Pro	Met 20	Cys	Ile	Tyr	Arg	Ser 25	Pro	Glu	Lys	Lys	Ala 30	Thr	Glu
Asp	Glu	Gly 35	Ser	Glu	Gln	Lys	Ile 40	Pro	Glu	Ala	Thr	Asn 45	Arg	Arg	Val
Trp	Glu 50	Leu	Ser	Lys	Ala	Asn 55	Ser	Arg	Phe	Ala	Thr 60	Thr	Phe	Tyr	Gln
His 65	Leu	Ala	Asp	Ser	Lys 70	Asn	Asp	Asn	Asp	Asn 75	Ile	Phe	Leu	Ser	Pro 80
Leu	Ser	Ile	Ser	Thr 85	Ala	Phe	Ala	Met	Thr 90	Lys	Leu	Gly	Ala	Cys 95	Asn
Asp	Thr	Leu	Gln 100	Gln	Leu	Met	Glu	Val 105	Phe	Lys	Phe	Asp	Thr 110	Ile	Ser
Glu	Lys	Thr 115	Ser	Asp	Gln	Ile	His 120	Phe	Phe	Phe	Ala	Lys 125	Leu	Asn	Cys
Arg	Leu	Tyr	Arg	Lys	Ala	Asn 135	Lys	Ser	Ser	Lys	Leu	Val 140	Ser	Ala	Asn
Arg 145	Leu	Phe	Gly	Asp	Lys 150	Ser	Leu	Thr	Phe	Asn 155	Glu	Thr	Tyr	Gln	Asp 160
Ile	Ser	Glu	Leu	Val 165	Tyr	Gly	Ala	Lys	Leu 170	Gln	Pro	Leu	Asp	Phe 175	Lys
Glu	Asn	Ala	Glu 180	Gln	Ser	Arg	Ala	Ala 185	Ile	Asn	Lys	Trp	Val 190	Ser	Asn
Lys	Thr	Glu 195	Gly	Arg	Ile	Thr	Asp 200	Val	Ile	Pro	Ser	Glu 205	Ala	Ile	Asn
Glu	Leu 210	Thr	Val	Leu	Val	Leu 215	Val	Asn	Thr	Ile	Tyr 220	Phe	Lys	Gly	Leu
Trp 225	Lys	Ser	Lys	Phe	Ser 230	Pro	Glu	Asn	Thr	Arg 235	Lys	Glu	Leu	Phe	Tyr 240
Lys	Ala	Asp	Gly	Glu 245	Ser	Cys	Ser	Ala	Ser 250	Met	Met	Tyr	Gln	Glu 255	Gly
Lys	Phe	Arg	Tyr 260	Arg	Arg	Val	Ala	Glu 265	Gly	Thr	Gln	Val	Leu 270	Glu	Leu
Pro	Phe	Lys 275	Gly	Asp	Asp	Ile	Thr 280	Met	Val	Leu	Ile	Leu 285	Pro	Lys	Pro
Glu	Lys 290	Ser	Leu	Ala	Lys	Val 295	Glu	Lys	Glu	Leu	Thr 300	Pro	Glu	Val	Leu
Gln 305	Glu	Trp	Leu	Asp	Glu 310	Leu	Glu	Glu	Met	Met 315	Leu	Val	Val	His	Met 320
Pro	Arg	Phe	Arg	Ile 325	Glu	Asp	Gly	Phe	Ser 330	Leu	Lys	Glu	Gln	Leu 335	Gln
Asp	Met	Gly	Leu 340	Val	Asp	Leu	Phe	Ser 345	Pro	Glu	Lys	Ser	Lys 350	Leu	Pro
Gly	Ile	Val 355	Ala	Glu	Gly	Arg	Asp 360	Asp	Leu	Tyr	Val	Ser 365	Asp	Ala	Phe
His 370	Lys	Ala	Phe	Leu	Glu	Val 375	Asn	Glu	Glu	Gly	Ser 380	Glu	Ala	Ala	Ala
Ser 385	Thr	Ala	Leu	Glu	Ala 390	His	Gly	Arg	Ser	Leu 395	Asn	Pro	Asn	Arg	Val 400
Thr	Phe	Lys	Ala	Asn 405	Arg	Pro	Phe	Leu	Val 410	Phe	Ile	Arg	Glu	Val 415	Pro
Leu	Asn	Thr	Ile 420	Ile	Phe	Met	Gly	Arg 425	Val	Ala	Asn	Pro	Cys 430	Val	Lys

246416_1.txt

<210> 87
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 87

His	Gly	Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro
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Met	Asn	Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu
			20					25					30		
Asp	Glu	Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val
		35					40					45			
Trp	Glu	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln
	50					55					60				
His	Leu	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro
65					70				75						80
Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn
				85					90					95	
Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser
			100					105					110		
Glu	Lys	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys
		115				120						125			
Arg	Leu	Tyr	Arg	Lys	Ala	Asn	Lys	Ser	Ser	Lys	Leu	Val	Ser	Ala	Asn
						135						140			
Arg	Leu	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp
145					150					155					160
Ile	Ser	Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys
				165					170					175	
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn
			180					185					190		
Lys	Thr	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn
		195					200					205			
Glu	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu
	210					215					220				
Trp	Lys	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr
225					230					235					240
Lys	Ala	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly
				245					250					255	
Lys	Phe	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu
			260					265					270		
Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro
		275					280					285			
Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu
	290					295					300				
Gln	Glu	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met
305					310					315					320
Pro	Arg	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln
				325					330					335	
Asp	Met	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro
			340					345					350		
Gly	Ile	Val	Ala	Glu	Gly	Arg	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	
		355					360				365				
His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala
	370					375					380				
Ser	Thr	Ala	Leu	Glu	Ala	Tyr	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val
385					390					395					400
Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro
				405					410					415	

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Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420 425 430

<210> 88
<211> 423
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 88

Arg	Asp	Ile	Pro	Val	Asn	Pro	Ile	Cys	Ile	Tyr	Arg	Asn	Pro	Glu	Lys
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Lys	Pro	Gln	Glu	Arg	Arg	Gly	Ala	Gly	Ala	Gly	Glu	Gly	Gln	Asp	Pro
		20						25					30		
Gly	Val	His	Lys	Pro	Pro	Val	Trp	Glu	Leu	Ser	Arg	Ala	Asn	Ser	Arg
		35					40					45			
Phe	Ala	Val	Val	Phe	Tyr	Lys	His	Leu	Ala	Asp	Ser	Lys	Asp	Asn	Glu
	50					55					60				
Glu	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met
65					70					75					80
Thr	Lys	Leu	Gly	Ala	Cys	Gly	Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val
				85					90					95	
Phe	Gln	Phe	Asp	Thr	Ile	Ser	Glu	Lys	Thr	Ser	Asp	Gln	Val	His	Phe
			100					105					110		
Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	Tyr	Lys	Lys	Ala	Asn	Lys	Ser
		115					120					125			
Ser	Glu	Leu	Ile	Ser	Ala	Asn	Arg	Leu	Phe	Gly	Glu	Lys	Ser	Leu	Val
	130					135					140				
Phe	Asn	Glu	Thr	Tyr	Gln	Asn	Ile	Ser	Glu	Ile	Val	Tyr	Gly	Ala	Lys
145					150					155					160
Leu	Trp	Pro	Leu	Asn	Phe	Lys	Glu	Lys	Pro	Glu	Leu	Ser	Arg	Lys	Ile
				165					170					175	
Ile	Asn	Glu	Trp	Val	Ala	Asn	Lys	Thr	Glu	Arg	Arg	Ile	Thr	Glu	Val
			180					185					190		
Ile	Pro	Glu	Lys	Gly	Ile	Asp	Asp	Leu	Thr	Val	Leu	Val	Leu	Val	Asn
		195					200					205			
Thr	Ile	Tyr	Phe	Lys	Gly	His	Trp	Lys	Ser	Gln	Phe	Pro	Ala	Pro	Asn
	210					215					220				
Thr	Arg	Leu	Asp	Leu	Phe	His	Lys	Ala	Asn	Gly	Glu	Thr	Cys	Asn	Val
225					230					235					240
Pro	Ile	Met	Tyr	Gln	Glu	Ser	Arg	Phe	Pro	Tyr	Ala	Phe	Ile	Gln	Glu
				245					250					255	
Asp	Lys	Val	Gln	Val	Leu	Glu	Leu	Pro	Tyr	Lys	Gly	Asp	Asp	Ile	Thr
			260					265					270		
Met	Val	Leu	Val	Leu	Pro	Lys	Ala	Gly	Thr	Pro	Leu	Val	Glu	Val	Glu
							280					285			
Arg	Asp	Leu	Thr	Ser	Asp	Lys	Leu	Gln	Asp	Trp	Ile	Asp	Ser	Met	Met
	290					295					300				
Glu	Val	Ser	Leu	Thr	Val	Ser	Phe	Pro	Arg	Phe	Arg	Val	Glu	Asp	Ser
305					310					315					320
Phe	Ser	Val	Lys	Glu	Lys	Leu	Arg	Lys	Met	Gly	Leu	Glu	Asp	Leu	Phe
				325					330					335	
Ser	Pro	Glu	Asn	Ala	Lys	Leu	Pro	Gly	Ile	Val	Ala	Gly	Asp	Arg	Thr
			340					345					350		
Asp	Leu	Tyr	Val	Ser	Glu	Ala	Phe	His	Lys	Ala	Phe	Leu	Glu	Val	Asn
		355					360					365			
Glu	Glu	Gly	Ser	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Val	Ile	Ser	Gly
		370				375					380				
Arg	Ser	Phe	Pro	Met	Asn	Arg	Ile	Ile	Phe	Glu	Ala	Asn	Arg	Pro	Phe

385 390 395 400
Leu Leu Phe Ile Arg Glu Ala Thr Leu Asn Thr Ile Ile Phe Met Gly
 405
Arg Ile Ser Asp Pro Cys Ser
 420

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<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct
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<400>	89														
Met 1	Tyr	Leu	Leu	Ser 5	Leu	Leu	Leu	Leu	Ser 10	Leu	Leu	Gly	Ser 15	Ala	Tyr
Leu	Gln	Pro	Gln 20	His	Ala	Asp	Ile	Cys 25	Leu	Ala	Lys	Pro 30	Lys 30	Asp	Ile
Pro	Leu	Thr 35	Pro	Met	Cys	Val	Tyr 40	Arg	Lys	Pro	Leu	Glu 45	Val	Val	Glu
Thr	Glu 50	Glu	Lys	Glu	Lys	Glu 55	Pro	Thr	Thr	Gln	Glu 60	Gln	Lys	Val	Pro
Glu 65	Ser	Thr	Asn	Pro	Arg 70	Val	Tyr	Glu	Leu	Ser 75	Gln	Ala	Asn	Ala	Lys 80
Phe	Ala	Ile	Ala	Phe 85	Tyr	Lys	Asn	Leu	Ala 90	Asp	Ser	Lys	Arg	Asp 95	Lys
Glu	Asn	Ile	Phe 100	Met	Ser	Pro	Leu	Ser 105	Ile	Ser	Gln	Ala	Phe 110	Thr	Met
Ala	Lys	Leu 115	Gly	Ala	Cys	Asn	Asn 120	Thr	Leu	Lys	Gln	Leu 125	Met	Glu	Val
Phe	His 130	Phe	Asp	Thr	Val	Ser 135	Glu	Arg	Ala	Ser	Asp 140	Gln	Ile	His	Tyr
Phe 145	Phe	Ala	Lys	Leu	Asn 150	Cys	Arg	Leu	Phe	Arg 155	Lys	Ala	Asn	Lys	Ser 160
Ser	Glu	Leu	Val	Ser 165	Val	Asn	Arg	Leu	Phe 170	Gly	Glu	Lys	Ser	Leu 175	Thr
Phe	Asn	Glu	Thr 180	Tyr	Gln	Asp	Ile	Ser 185	Glu	Ile	Val	Tyr	Gly 190	Ala	Lys
Leu	Trp	Pro 195	Leu	Asn	Phe	Arg	Asp 200	Lys	Pro	Glu	Leu	Ser 205	Arg	Glu	Ile
Ile	Asn 210	Asn	Trp	Val	Ser	Asn 215	Lys	Thr	Glu	Lys	Arg 220	Ile	Thr	Asp	Val
Ile 225	Pro	Lys	Asp	Ala	Ile 230	Thr	Pro	Asp	Thr	Val 235	Leu	Val	Leu	Ile	Asn 240
Ala	Ile	Tyr	Phe	Lys 245	Gly	Leu	Trp	Lys	Ser 250	Lys	Phe	Asn	Ser	Glu 255	Asn
Thr	Lys	Met	Asp 260	Gln	Phe	His	Pro	Ala 265	Lys	Asn	Ser	Asn	Cys 270	Leu	Thr
Ala	Thr	Met 275	Tyr	Gln	Glu	Gly	Thr 280	Phe	Arg	Tyr	Gly	Ser 285	Phe	Lys	Asp
Asp	Gly 290	Val	Gln	Val	Leu	Glu 295	Leu	Pro	Tyr	Lys	Gly 300	Asp	Asp	Ile	Thr
Met 305	Val	Leu	Val	Leu	Pro 310	Ser	Gln	Glu	Thr	Pro 315	Leu	Thr	Thr	Val	Glu 320
Gln	Asn	Leu	Thr	Leu 325	Glu	Lys	Leu	Gly	Asn 330	Trp	Leu	Gln	Lys	Ser 335	Arg
Glu	Leu	Gln	Leu 340	Ser	Val	Tyr	Leu	Pro 345	Arg	Phe	Arg	Val	Glu 350	Asp	Ser
Phe	Ser	Val 355	Lys	Glu	Lys	Leu	Gln 360	Glu	Met	Gly	Leu	Val 365	Asp	Leu	Phe

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Asp Pro Asn Ser Ala Lys Leu Pro Gly Ile Ile Ala Gly Gly Arg Thr
 370 375 380
 Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn
 385 390 395 400
 Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Ile Leu Thr Gly
 405 410 415
 Arg Ser Leu Asn Leu Asn Arg Ile Ile Phe Arg Ala Asn Arg Pro Phe
 420 425 430
 Leu Val Phe Ile Arg Glu Val Ala Ile Asn Ala Ile Leu Phe Met Gly
 435 440 445
 Arg Val Ala Asn Pro Cys Thr Glu
 450 455

<210> 90

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 90

Met Tyr Ser Pro Gly Ala Gly Ser Gly Ala Ala Gly Glu Arg Lys Leu
 1 5 10 15
 Cys Leu Leu Ser Leu Leu Leu Ile Gly Ala Leu Gly Cys Ala Ile Cys
 20 25 30
 His Gly Asn Pro Val Asp Asp Ile Cys Ile Ala Lys Pro Arg Asp Ile
 35 40 45
 Pro Val Asn Pro Leu Cys Ile Tyr Arg Ser Pro Gly Lys Lys Ala Thr
 50 55 60
 Glu Glu Asp Gly Ser Glu Gln Lys Val Pro Glu Ala Thr Asn Arg Arg
 65 70 75 80
 Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Asn Phe Tyr
 85 90 95
 Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser
 100 105 110
 Pro Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys
 115 120 125
 Asn Asp Thr Leu Lys Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile
 130 135 140
 Ser Glu Lys Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn
 145 150 155 160
 Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Asp Leu Val Ser Ala
 165 170 175
 Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Ser Tyr Gln
 180 185 190
 Asp Val Ser Glu Val Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
 195 200 205
 Lys Glu Asn Pro Glu Gln Ser Arg Val Thr Ile Asn Asn Trp Val Ala
 210 215 220
 Asn Lys Thr Glu Gly Arg Ile Lys Asp Val Ile Pro Gln Gly Ala Ile
 225 230 235 240
 Asn Glu Leu Thr Ala Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly
 245 250 255
 Leu Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Pro Phe
 260 265 270
 Tyr Lys Val Asp Gly Gln Ser Cys Pro Val Pro Met Met Tyr Gln Glu
 275 280 285
 Gly Lys Phe Lys Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu
 290 295 300
 Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys

246416_1.txt

305	Pro	Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Gln	Glu	Leu	Thr	Pro	Glu	Leu
					325					330					335	
	Leu	Gln	Glu	Trp	Leu	Asp	Glu	Leu	Ser	Glu	Thr	Met	Leu	Val	Val	His
			340						345					350		
	Met	Pro	Arg	Phe	Arg	Thr	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu
			355					360					365			
	Gln	Asp	Met	Gly	Leu	Ile	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Gln	Leu
		370					375					380				
	Pro	Gly	Ile	Val	Ala	Gly	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala
	385					390					395					400
	Phe	His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala
				405					410						415	
	Ala	Ser	Thr	Ser	Val	Val	Ile	Thr	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg
				420					425					430		
	Val	Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Leu	Ile	Arg	Glu	Val
			435					440					445			
	Ala	Leu	Asn	Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val
		450				455						460				

Asn
465

<210> 91
 <211> 1599
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 91

caccagc	atctcctcca	attcatccag	ctactctgcc	catgaagata	atagttttca	60
ggcggattgc	ctcagatcac	actatctcca	cttgcccagc	cctgtggaag	attagcggcc	120
atgtattcca	atgtgatagg	aactgtaacc	tctggaaaaa	ggaagggtta	tcttttgtcc	180
ttgctgctca	ttggcttctg	ggactgctgt	acctgtcacg	ggagccctgt	ggacatctgc	240
acagccaagc	cgcgggacat	tcccatgaat	cccattgtgca	tttaccgctc	cccggagaag	300
aaggcaactg	aggatgaggg	ctcagaacag	aagatcccgg	aggccacca	ccggcgtgtc	360
tgggaactgt	ccaaggccaa	ttcccgtttt	gctaccactt	tctatcagca	cctggcagat	420
tccaagaatg	acaatgataa	cattttcctg	tcacccctga	gtatctccac	ggcttttgc	480
atgaccaagc	tgggtgcctg	taatgacacc	ctccagcaac	tgatggaggt	atttaagttt	540
gacaccatat	ctgagaaaac	atctgatcag	atccactttc	tctttgcca	actgaactgc	600
cgactctatc	gaaaagccaa	caaatcctcc	aagttagtat	cagccaatcg	cctttttgga	660
gacaaatccc	ttaccttcaa	tgagacctac	caggacatca	gtgagttggt	atatggagcc	720
aagctccagc	ccctggactt	caaggaaaat	gcagagcaat	ccagagcggc	catcaacaaa	780
tgggtgtcca	ataagaccga	aggccgaatc	accgatgtca	ttccctcggg	agccatcaat	840
gagctcactg	ttctggtgct	ggttaacacc	atttacttta	agggcctgtg	gaagtcaaag	900
ttcagccctg	agaacacaag	gaaggaaactg	ttctacaagg	ctgatggaga	gtcgtgttca	960
gcattctatga	tgtaccagga	aggcaagttc	cgttatcggc	gcgtggctga	aggcaccag	1020
gtgcttgagt	tgcccttcaa	aggatgatgac	atcaccatgg	tctctatctt	gcccaagcct	1080
gagaagagcc	tggccaagggt	ggagaaggaa	ctcaccaccag	aggtgctgca	ggagtggctg	1140
gatgaattgg	aggagatgat	gctggtggtt	cacatgcccc	gcttccgcat	tgaggacggc	1200
ttcagtttga	aggagcagct	gcaagacatg	ggccttgctg	atctgttcag	ccctgaaaag	1260
tccaaactcc	cagggtattgt	tgcagaaggc	cgagatgacc	tctatgtctc	agatgcattc	1320
cataaggcat	ttcttgagggt	aaatgaagaa	ggcagtgaa	cagctgcaag	taccgctggt	1380
gtgattgctg	gccgttcgct	aaaccccaac	aggggtgactt	tcaaggccaa	caggcccttc	1440
ctggttttta	taagagaagt	tcctctgaac	actattatct	tcatgggcag	agtagccaac	1500
ccttggtgta	agtaaaatgt	tcttattctt	tgcacctctt	cctatttttg	gtttgtgaac	1560
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<210> 92
 <211> 430
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT

<222> (386)...(389)

<223> Xaa = any amino acid

<400> 92

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
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Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
		35					40					45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
	50					55					60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser
65					70					75					80
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
				85					90					95	
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
			100					105					110		
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu
		115					120					125			
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg	Leu
	130					135					140				
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser
145					150					155					160
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu	Asn
				165					170					175	
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys	Thr
			180					185					190		
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu	Leu
		195					200					205			
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys
	210					215					220				
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala
225					230					235					240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys	Phe
				245					250					255	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro	Phe
			260					265					270		
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu	Lys
		275					280					285			
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
	290					295					300				
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg
305					310					315					320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp	Met
				325					330					335	
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly	Ile
			340					345					350		
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys
		355					360					365			
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr
	370					375					380				
Ala	Xaa	Xaa	Xaa	Xaa	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe
385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	

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Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 93

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 93

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
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Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
		35					40					45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
	50					55					60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser
65				70						75					80
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
				85					90					95	
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
			100					105					110		
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu
		115					120					125			
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg	Leu
		130				135					140				
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser
145					150					155					160
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu	Asn
				165					170					175	
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys	Thr
			180					185					190		
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu	Leu
		195					200					205			
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys
	210					215					220				
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala
225					230					235					240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys	Phe
				245					250					255	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro	Phe
			260					265					270		
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu	Lys
		275					280					285			
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
	290					295					300				
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg
305					310					315					320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp	Met
				325					330					335	
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly	Ile
			340					345					350		
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys
		355					360					365			
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr
	370					375					380				
Ala	Val	Val	Ile	Ala	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe

246416_1.txt

385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys		
			420					425					430		